

054030-0031nonactincluster.ST25.txt
SEQUENCE LISTING

<110> Shen, Ben
Hyung-Jin, Kwon

<120> METHODS OF DIRECTING C-O BOND FORMATION UTILIZING A TYPE II
POLYKETIDE SYNTHASE SYSTEM

<130> 054030-0031

<150> US 60/405,245
<151> 2002-08-22

<160> 7

<170> PatentIn version 3.2

<210> 1
<211> 15559

<212> DNA

<213> Streptomyces griseus

<400> 1
ctcaggcgcg cggtaaacag caccatcctg cggcgccctgg tgcgc(cc)ga ggagatcgcc 60
gcccagggtcc ttttcctgct ctccgacctc tccggcgggaa tgaccggaca ggccgtcaac 120
gtggacgcgg gggctctgtg agcaaggagc acggccccgg gaaggggcgaa ccgc(cc)tc 180
cgaaacagct gctcgcccccc gcggcgccgc cctgggcccccc cgccccccgg gacgcgttgg 240
tcaccggat ggggttctgc ctgcccgttgg cgggcgacga gccgggtgcgc acggccgagc 300
aggcttgggc ggccgcctcc accgggacca gtcatgtcga acgcgacggc ttccaccacg 360
ggaccgtacg cggtgccgcg gaggcggtcg gagagctgct gccggacata ccggcccgct 420
atctgcgcag ctacgcccac gtccacctct acgggctgat ctcgtggcc gaggcctgcc 480
gggacgcggg actcgattac gggaaaggcg agttgagagg ggcggacgtg ctgaccgcgg 540
gggcgggggt ggacagcaac tacgacagct accgcgcctg gcacgcacgc gatccggcga 600
cggtcactcc ctcggacgc aagtccctct tcgtacggct cctgggtggcg ggcaccccca 660
gacgtcgccggg ccccgccatccag gccgcgcgtc tcgggtccac cggcgccaa tacacgggtga 720
gctgcggctg cgcctccctcc tcgggtcgctc tcggcatcgcc cccgcgtatg atgcctccg 780
gccagagcga cctgggtcgatg gtcaccgggg tggaccgctt cgacaccgaa cgggtcgatg 840
acggacaccg gttgcgcgag gtcgtcgagc gcgaggggcgatg gacgggtgcgg cacaacagcg 900
atccgcggc acgcacccgt cacgaccggc cgatgcgcgc gtacgcacgc gcgccgcact 960
gcatgaacta cggcgacggg tcgggtaccc tgcgttggaa gagccgcgaa cacgcgcgg 1020
cgccggggcgcc cccggacgcac ggggcgggtcc tcggccaggc caccacgcgc gggggccctga 1080
acagcgccgt cgccatcgac accggcggtt cggggctggc cgaagcgcc cggccgcggcc 1140
tggcgacca tacctcgctg gggcgatcc cctacgtcaa cggggcgcc gaggcgacg 1200

054030-0031nonactincluster.ST25.txt

cgctgtcac	ccggatcgag	tccaacgccc	tccgcgcctt	gtggggcgac	cggtccgagc	1260
aggtgcttgt	gagttcgag	gaggcgtgct	tcgggcacag	cggcgcgccc	ctcggaatc	1320
tgggcacggc	gctgacgctg	atgatgatgc	gcgagggaga	ggtctgcccc	acggccaaact	1380
gcgcgacccc	gtcgcccg	tgcacattcg	accgggtccc	cggcaccagg	acgcgtgcgc	1440
tgggcattcga	ccggggccctg	agcttcaact	accagggtggg	cggggtcac	agcgcactgc	1500
tgctgggagg	tggcgatgtc	tgctgagctg	cctctgctgc	ggcttccgg	cgcgggttc	1560
gtcctgcgg	ggccggacgg	ccgcgcctgc	accgacctgg	acaccttctg	gggtgtggtg	1620
cgcgacgggg	cgagctgcct	ctccccgtac	gcccatccc	aactccccct	ccgtatcgcc	1680
gggaccgtga	acggctggga	cccgagacc	gaactccgc	tgtcggaaacg	gcagatacgc	1740
cgttcctcgc	gcgcgggct	gatggccacg	ggtgcggtgc	accgggcgt	ggagcacgccc	1800
gggctgagcg	cggacgacct	cgatccgggg	cgtaccgcgc	tcgtcgcctg	ctcgctccag	1860
ttcgcgttcc	cggagaccga	gcgctactac	gccctggccc	gggacgaggg	ggtcgcccgc	1920
ctcggcatgg	agtactggct	caacgggacc	ccgcccagtg	tggtgggcac	cgtggcctcc	1980
ggcctccggc	tgcctgcca	gacgctgagc	gtggcgggct	cctgcaatgt	ggcgcgtcg	2040
acgctccacc	tgcgtccagca	gatgttccgg	tgcggggaca	tcgaccgcgc	gatcgtcg	2100
ggcgtggaca	ccacgggtgga	cccggtttc	gtggcaggca	ccagccacac	cggacgcagc	2160
ggctaccgcg	cgtcctcgct	ctccgacac	cccggcgcac	tccggccgca	cgacgagatc	2220
cagacccggca	acgcccacgg	ggagggcgcg	ctcgggtgg	tgcggaaaa	ccggcggcgc	2280
accggggacc	gcccgggct	gctgcaccgc	gcgcacatgc	gcacctcg	ctccaacggc	2340
ccctccaccg	tggccaccgg	accgcccccc	aacgtgggtgg	gcgcacgtact	ggccacgctg	2400
gcttcggccc	ggcgcggcct	ggcgatctg	gcgttcgtca	acgactacgc	ggacggcaac	2460
cggttcgtcg	aggaccac	gtgccaggcg	ctcgggggg	tgcgggggg	ggccgggtac	2520
ggcggggagc	tgcggctcac	caaccaggag	gcggtcttg	ggcatgtcg	cggacccggc	2580
ggcctggta	aactcctcg	cagcctcc	atgcgtcg	acggccatat	cgcggcc	2640
gccaacaccc	tggtcccgt	cgcgggtctg	ccgggcgacc	cggtgctcg	ggcggcc	2700
gcgacccggc	gagacagcgc	gctgggtctc	gcctccgggg	ccggcggcga	cgcacgcagc	2760
atggtcatcg	aatacgaagg	cggcgacttgc	ccatgaccca	cgttgcac	acggcgcacgc	2820
ggccggggac	ggccgcggga	ggggacccgt	cgcgggcgc	ggtcagcacc	cgcgtgg	2880
tcgacgcgc	cggggggcgac	ggtcctggcg	ccggggccct	ctccgacgc	ctcaccgc	2940
tcggcctcg	ccccgaggcc	ccggacacccg	aggccccgga	caccggccgc	gccgattcc	3000
gcgacccccc	cccgccgc	tactgcgtc	tgctgctcg	cgaggaggcg	tacggcgc	3060
gacgctcg	ggccctggac	cgctcacgc	tccggccgc	cgcgtggcg	attgcggcg	3120

054030-0031nonactincluster.ST25.txt

cgggccccggg acggctcgtc ctggtgaccg acgcgacggg cgagacccac gccggaaccg	3180
accccgaccg gtacgcgcgg ctcgcccgg accgggcctg gtggcagcac ctggtcaccg	3240
aggtgtggcg ggcgcggcg tc accggcaaca ccgtggtcac gggctactcc cccggcctgg	3300
gccaccggct gtccgcccgg gcccggccgg ggctgctgcg ctgtctcgtg cagcgcggc	3360
ccaccacggc cgccgatgtc gcggccaccg tcgccttcct ggtctccggag gggtgttcgt	3420
acctggtcgg cgagactctg ccggtcgacg ggggcgcggg cctcggccag atcccgtccc	3480
tgcccggcg cccgcccacg acggcccccgg caccgcgcgg cggtgctccg cgggagcagc	3540
cgccgcccga gccgggtgagc ggtcaggacc tcctgggcca caaggtcctg gtggcggcg	3600
cgagcagcgg catcggccgg gccgcggcccc tgcacccctggc cggacgcggg gccgacgtga	3660
tcctggccgc cgcgggacg caggcgcctgg aggaggtggc cgccgagatc gaggcccggg	3720
gccggcaggc ctggaccctg cgctgcgacc tctccgacgc cgaggacgccc gcttctctgg	3780
gcgaacgggc ctggaaaggcg gccgacggcg tcaccgcct gctgtacgcg gcggggcacc	3840
tgggcttcag cgccggcggc ggccggcccg cttccgcgc cccgaccccttc gcggtaacc	3900
tgcacagctt cgtcgccgtc accgagtacc tggcggcccg ctggcgggac gagaggatgc	3960
ccggagcggg ggtcggggtc tcctcggtca gctccacgc cagccgggtg gcgggcctgg	4020
agtactacgg ggccgagcaag gccgcgatgg cgccgatcat ccgcgtgtc gcggtctcgg	4080
tgggcccaca cggcatccgc gccaactgcg tggctcccg catcatcgag acgcccgtatgg	4140
gcgcacgcggc ggggccccgac caccggcgcg gctggatcag ccggataccg gccgggcggg	4200
tcggcgcaccc gcacgagggtg gcggcggtcc tcggctatct gctgagcggc tcggcctccc	4260
gggtgaccgg tgccgtctg cgccgcggacg gcggcttcgg cctcggtgac gtggctccgc	4320
tgcggccggg atacccggag cgggccttcc ctgcaccggc gctccggag cggcggagg	4380
gggagaaccg atgaccgcca ccgcgcgaacg aggcccccac ccggctgcgg tcgtcgccgg	4440
cgcctccctcc gggatcgggg ccgcgtcgc ccgcgcactg gccgcgcgcg gcagcgcgt	4500
ggcgctggtc gggcggcggg agcccggact gaaggaggtc gcggagtcga tccgcgcggc	4560
cggcggaaacc gcgcgttcgc tcgccttggc cctggccggg ccgggtgccc ccgcgcaggc	4620
ggtcggccgc accgcggccg gactggggcc ggtcgggctg ctgggttgca gcgcggcgc	4680
catccggctg gccgcgtcc acgagaccga ggagcggcac tggaaacggc agttgcgggt	4740
gaacctcactg gtgcgttcc tgctggcccg tgagggtctg cccggcatgc gggagcgcgg	4800
tttcggctgg gtcgtgaaca tcggctccgg tgtggctcg gaggtggtgc cggcagcgg	4860
cggctacggc gtcagcaacg acaccgtca ccggctcacc gagctgatcc acgaggagaa	4920
ccgcgacctc gggatccgcg cggtcaccgt cggccgggc tgggtctcca cccggctcgc	4980

054030-0031nonactincluster.ST25.txt

ggcccgcccc	gccgatctcg	gggtgcccga	ggaggaggtg	ctggacgcgg	aggacatgc	5040
ggacaccgtc	gcgtggctgc	tggaccgtcc	ggcccgatg	agcgtcggcc	cgctggtccg	5100
cgtcgagccc	tcggcgagcc	ggccgcgcgc	cggtgacgcc	atgaccgc	atctgaccg	5160
ttcccgcgcc	gagggcgccg	gaccggatgc	tgaggagacc	cgctgatggg	caggaccacc	5220
ctcatcgagc	acgacgtgcc	ggtggagatg	cgcgacggga	cgglyctgcg	ggccgatgtg	5280
tggcgccccg	ccgaaggacc	ggcctcgccc	gccgtgctct	tccgcacccc	gtacggcaag	5340
tccccgctgg	gtcttgccac	cctgaccccg	gcccagtgcg	tggaccgggg	gtacgcggcg	5400
gtcgtgcagg	acacccgggg	ccggttcggc	tcggagggcg	agtgggcgcc	gctggactgg	5460
tcccaggagg	ggcccacgg	gtacgacacc	gtcgagtgg	ccgccaaca	gccttggtgc	5520
gacggaaacg	tggccatggc	gggcacctcg	taccaggcga	tcgtccagtg	gctggccgcc	5580
atggagaagc	cgcgcaccc	gcggggccatc	gcgcacca	tgtccaccc	ggcccccttc	5640
gacgcccagc	agtcggcg	tttcctgcgg	ctggaccacc	tcacgagctg	gctcggcctg	5700
accgcgctgg	agtgggtgca	gcgcccggcg	gcggcggcg	atccggtg	cggggcggtc	5760
gtcgccgagg	tcgtgcagct	gctcaccgca	cccgaagtgc	cgctgcgc	ctggccgtt	5820
tcgaccatcc	tcgacttcga	ggggtttccc	ggccggctgc	gggacatctt	cgcggggcac	5880
gtggcgacgg	tggccacta	ccacctcggg	gaagtcgggg	tgcccacctt	ctcggtcggc	5940
ggctggta	acgtgttctc	ccacggcacg	atcgagctgc	accgcgcgt	gcgcgcctg	6000
gaccgggtgg	cgggacggca	cgagctgg	gtcgaccct	gggtgcactc	gggtcaactg	6060
cccgagg	agggcgaggt	gaacacgggg	ccctacgg	cggcgcagg	cgcacggctg	6120
gccgatctgc	acctggactt	cttcgaccgc	catctacgg	cgccgggggg	gacgacgggc	6180
cgggactccg	gcggggacgt	gcggattttc	cttcgcgg	atgacgcctg	gcaccggg	6240
gcgagctggc	cgcgc	ggccgtc	gcgcctgg	acctggcgg	tccggccac	6300
ggcgaggagg	gcggcagg	gctgccc	ccgcgggg	aggccccgg	ccacgacgc	6360
ttcacctacg	acccggagga	cccggtgccc	tcgcacgg	ggcgggt	ccagctcgg	6420
aggctggcgg	cggggccgt	caaccagg	catctggagg	acaggccg	cgtgctc	6480
tacaccc	agccgctac	cgagcc	gacgc	gccggcag	gtgcgg	6540
cgcttcgg	cggacgcacc	cgcac	gtgg	tcgca	aactcacc	6600
gacgggcgtt	cgctgctcg	ggccgagg	agcctcc	tggagg	ggggacgg	6660
ccgcgggacg	agccgtacga	cgcgc	ctgctc	acaccgc	gcgc	6720
cccgccacc	ggctgcgggt	ccacgtacc	agcagca	tccccc	atcttgg	6780
cccaacatcc	cgggcccgt	cg	gactg	gcacc	ccagtcgg	6840
tggtacggcg	gcccgtacga	gagcgt	cg	ccctgccc	gccgagc	6900

054030-0031nonactincluster.ST25.txt

ggggagaccg	cgtgatcgac	gatgtgctcg	atccggcgtc	cggccgcgtg	cccacggcgg	6960
agcagtgcgt	gctgggtccc	ctgctcaggc	gacgtgccgc	cgcagcaccc	gcggcgccgt	7020
acgcgttgat	gccggacggt	gacctctgga	cgtacgcgcg	caccctccgg	gagaccgagg	7080
agacggccgc	cgcgtccag	gcgctggag	tcgtcccccgg	cgaactgggt	ctgagctggc	7140
tgccaacgg	acccgacgcg	ctgcgcgcct	ggtacgggt	caacctggcg	ggcgcggtcc	7200
tggtgccgct	caacatcgcc	taccgggtg	cgatcctgcg	tcaggtgate	gccgacagcg	7260
gggcccgggt	gctgatctgc	cggccgtcgc	tggcggccccg	gctggaggat	tcggacgacg	7320
cggtgggggc	ggtgcgcacg	gtggtcctgc	tgccggggcc	cgaggacgcg	gcccaggacg	7380
tggaggcgct	cgcggggcgg	ctggccacgc	gcttccgggt	ggagaccgca	ctgcgcgcgg	7440
accgggcgga	gttcgcggag	ccggtgcccg	ccccccggcc	gtgggacccg	cagaccgtca	7500
tctacaccc	cgggacgacc	ggtccgtcca	agggcgtcgt	ctccctctac	gcgcacccgt	7560
acagcagttg	caccgcgcg	ttccacggca	tggccggacc	ggaggaccgc	tatctgctgc	7620
aactgcccgt	gttccacgcg	ggcggcacga	tcggcgcgta	cgggatgcg	gtgcacggcg	7680
gttcggtgac	ggtcgtgccc	gcgttacca	ccggggagtt	ctggccgctg	atccggcgga	7740
cggggacgac	cctgtgcacg	ctgctcggcg	tgtggcgac	ctatctgctc	aagcagccgc	7800
cgctgcgcga	ggacaccgcg	caccctgtgc	ggggcccta	cgtcatcccg	ttcaccgagg	7860
gggcgacgga	gttctccaag	cggttcgggg	tcccggtccg	cgcgtgttc	aacatgaccg	7920
aggtgtcgt	tccggtgctc	tccgcgcgg	accaccaccc	gggcgtcccg	atgcactgcg	7980
gggagccccc	gccggggatc	gccgcgcgg	tcgtcgacga	ccacgaccgg	gaggtggcg	8040
acggcgaggc	gggcgaactg	gtgctgcgcg	cggaccgtcc	gtggtcgttc	ctgagcggct	8100
acctcggccg	gccccccgag	acggccgccc	tctggcgcaa	cggctggttc	cacaccgggg	8160
acaccctccg	cggggccccc	gacggcgggc	tggtcttcgt	ggaccgcaag	aaggacgcca	8220
tccgcaggcg	cggcgagaac	atctccctct	tcgaggtgga	ggcgcaggcg	gtggcccacc	8280
cgggggtgct	ggaggcggcg	gcggtggcg	tgcccgcgaa	cgagggcgag	gacgaggtgc	8340
tgctggtggt	ggcggaccgc	gaccctcgg	ccccggtcga	cccggcggcg	ctgctggagt	8400
tcctgcggga	gcccgtggcc	cacttcatgc	tgcccgcta	catccgggt	ctgcccggac	8460
tcccgaagac	tcccaccggc	aagccgacca	agcacacgc	gcgcgcggag	ggcgtggtgg	8520
cggggacgtg	ggaccgcgag	gccgcggca	tccggatacg	cagggagaag	atcgtatgaa	8580
ccaggaagca	ttccggggcg	gccaggaacc	cccggccgag	tgggcggggg	cggcgaccga	8640
gtcgttcgcg	gacttcgcgc	accgggtgga	cggcaaggag	gtcgtaccgc	tgcggccctc	8700
gcttgcgggc	ggggtcgcca	ccctgacgct	ggaccggccg	caccgcgcga	acagccctcg	8760

054030-0031nonactincluster.ST25.txt

tcccgaggc caccggccgc ctcttcgct acctcctgct gcgcaacaag ccgggtggacc 10740
tcgacaccat gacccgcgaa ctcgccagg ccaagagcgg gctgagtgtg gccgcccccc 10800
aactggaggc ctggtccctg gtgcggcgct cgaccaggc cgccagcagg cgatcgact 10860
acgaggcggt gggcgacctc cagcacctgc tgctggtaa caacgcccatt atgcgcaagt 10920
tcaccgagac gctgagctcg ggaatcccg tggcgcgcgg cgaggcccg gaccgactgg 10980
cctcgctcgc cgccctgttc aacgggtacg tggagcagac cgaggcgctg gtggccgcct 11040
gggaggcccg gcgcgcgcgc acctgagccc ggccgttccc ttctcccttc tgagcccgcc 11100
cgttctcttc tccctcccttcc tccgcttccct cgtccttccc cttcctgttcc ccgtatggagt 11160
gaccgtgaac gtgtcgtccg tccccgcgcc gggcaacggaa acaacgggtgg ccaccgcgt 11220
ggcggaccct ggagtccgga tccgcccgcgg ggtcatggac gcctgctcgc tgggtgtacga 11280
cgacgcgggc tggcgggcgt acctgaaccg gctggcgag aacgcccctg agtacctggaa 11340
tgtcttctcc gcctcgttcttcc gccgggtactt cggccctcgc cacaccgcgt accgcgacgc 11400
gctcgcgcgc cggccggcagg acgcgatcga cgtgtccctg ccaccggacc ggccaccgtt 11460
cgatctggcc gggcatctcg cggaccggaa acggcagggt gtgacgggcg agttcgccat 11520
gggctcggcg gaacggctcgc cggacggccg tacggtaaac gagtggtcgc tggagaccgt 11580
acgggacgtg cgacggccgaa tccacgtctg ggccgggatc tccctgcgcg accccgcgc 11640
cgcgctgcgg gagctggagc ggctgctggc ggccggggcg accgggctgt gcgtcatccc 11700
cttcctggac ggcacccgacc cggccgaccc gaggttcgccc ccggctctggg acggccgcggc 11760
cgaggcgcgg ctgcccgttcc ggctgcacac cggccaccac ttcgcccggaa gccaccccg 11820
cggctgggc agctggcgta cggtcgagac gctcgcggc cggccaccgcg cgctgctgt 11880
cgtcgcggcgg cacgcgggct ggcccgatgt gcaggagatg ctgctcacgg ccggccggca 11940
ccccggggtc ttccctggagt tctccctcgca ccggcccccgg cacatgtcca agcccggttc 12000
gggctgggag cccctgctgc accacgccccg gggatggcc cggacccggg tcgttccgg 12060
cacctcgacc tgggtcaatc cggggccgac gggaccgctg gccgatgagc tggccgcgt 12120
cccgctcccc gccgacgtgg tcgcccgttcc gctctgggc aacgcggagg cgctggtcgc 12180
ccgtgcggcc gggacccacc ggggctgagc cggccggggaa gccctccggaa tggatgcggac 12240
ccgtgcgcgg gggcaggggaa tccgcccggac ggccgaaagc cgcagccccc tcggaaagcct 12300
cttcctggca cacgtggca ggaggcggat cctggccggg ccggccctac cgtcggcgt 12360
gtcagccacc ccgaccaacg gagatgtacg acatggcaaa gatccttttc gtgggtcgc 12420
gcgcggacca ctggaccctg gcggacggca cggccaccac cacgggcttc tggggccgagg 12480
aggccgtggc gccgttaccgg gcgttaccgg acgcggggca cgagggtggtc gtgcgcaccc 12540

054030-0031nonactincluster.ST25.txt

cgggcggcgt cgtcccgacc gtggaccggg gcagcctggc gcccacgtc aacggcgggc 12600
 aggagggcgc cgacgcggtg gcggccggtc ttgaggcggt cgaggagctg cggcggccgg 12660
 tcgcccggaa ggacgtggac ccggacgtgt acgacgcgtt cttctacccc ggcggccacg 12720
 gcccgtggaa ggacgtcgcg gtggaccccg tctccggcg gctgctcgcc cgggtgctgg 12780
 ctccggcaaa gccgctcgcc gtggctcgcc acyggcccgcc ggcgtcgctg gccgcgacccg 12840
 gacccgacgg ccgggtcccg ttcgcccgggt atcggctgac gggcttcacc aacgcccagg 12900
 aggcccaggc gggcttcgac gacaaggcga agtggctgct ccaggaccgg ctggtggcgc 12960
 tgggcgcgaa ctccaggaa ggtgagccct gggcgccgtt cgtcatcacc gaccggaacc 13020
 tgatcacggg tcagaacccg gcctccccc tcccgttggc cggcgaactg ctcaacccggc 13080
 tcggctgacc ggccgatcgg cgggtcccgccc cccggccggc cgggctgttc agacccagtc 13140
 cccggcgcg ggcggctcgc agagctccag caccaccggc cccgtctcggt gctcgcccc 13200
 ggagacgggc cggacgcgcg caccgaccgt caccagggtc ggagccgccc ccacgatctg 13260
 gcagcggaaag acgaacccctt ccgagaaccg caccaggac tcggtgcgcg cagcctcggt 13320
 atagcggtgg accacggcgg tccggacgac cacggcgtgg ccgggtggtgc gttcgggctc 13380
 cagttcgctc gacgcgcaca ccgggcacag cagccgcggg aacgaggcgg tgccgcacca 13440
 gcggcagcga ttgttaggaga ggccgcactc ctcgtgcgcc ttctggacgg tgcccattgc 13500
 tgtctggac acggctcgac cccctgcgtcgact cgactcgac ggcggccacc tgcaactgcgg 13560
 gcgcgtccgc accatatggc actcagtgcc ggaccgtaaa ggcactgagt gcccattgg 13620
 actcagttct cggcgcacggc tgcctcgatc tgctgcacga cacgcccacat cgggtgccc 13680
 ttccgcgcga ccatcacgat cacccccc ttcccgccgc cggcaccggaa gaccggaaag 13740
 ggggtggccg gtgtggggac ggcaggccgc ccccacaccc tctcgaccgg ggcgagcgc 13800
 tgatccacag cccgcctcgaa gtcgcccgc cggccgcgaac gcagccacag ccgaagcccg 13860
 ttgttgtgcg cggcgcaccac cgaagcggcg atcacctcg cccgcagctc cccgtcgca 13920
 ccctcgccga agcgaccccg cagatgtcccg gcgagagtct gttcgtaacg ggcgcaccacc 13980
 gacagttcgat acgtccgcag ccccgacc tcccgagtga ggcggtagcg ctgcacggag 14040
 aactcgggtt tggccgcgtt catccgcacgc acgatgcgcg cggcgtcgca caccgcgcgg 14100
 accgggtcgac tgcgtcgac ggcggccagg aactcgggtcg tctcgccgag gcagcgtcg 14160
 tggtccggaa agaccgcgtc ctccttggac gggaaagtgc ggaagaacga acgcccggccc 14220
 accccggcca gcgcgcacgtat gtcgtccacg gtcgtccgtcg cgaagccccc ctccaggaaag 14280
 agccggaaagg ccgcctgtgc gagcacctcc cgcatgggtg ctttcttctc ggatcctcg 14340
 gcctcgctca tgcggcgaaa cgtagcaccg cgaggaggat tttggcactg cgtacctta 14400
 cagagggta ctagtgcgtt aatctctcca tcagtagcggaa tgacacccag gtgggaccac 14460

054030-0031nonactincluster.ST25.txt

acccaggtag	gcaggagagc	cggcgtgagc	ttgaggatcg	ttgtctgtgt	gaagtacgtg	14520
cccgacgcga	ccggtgaccg	gcgttgcgcc	gatgaccta	cgctggaccg	tgaggatgtc	14580
gacggtctgt	tgtcgagct	ggacgagta	gcggcgagc	aggcgttca	gatcgctgac	14640
ggggccggarg	atgcggagat	caccgtggt	acgggtggtc	cgaggatgc	caaggacgcg	14700
ttgcgcagg	cgttgcgtat	gggtgcggac	aaggcggttc	acgtcgagga	cgacgatctg	14760
cacggcagt	atgtgatggg	gacgtcgctg	gtgctggca	aggctgtgga	gaaggccggg	14820
tatgacctgg	tgatctgtgg	gatggcgtcg	acggacggtg	tgatgggtgt	gctgccggcg	14880
ttgctggcgg	agcgtctggg	tgtgcccgag	gtgacgttgc	tgtccgaggt	cgcggtgac	14940
ggtgtgttgg	tgacggggcg	gcgtgacggt	gacacggcg	ccgagcagct	tgaggcgtcg	15000
cttcccgccg	tgggtcggt	gaccgaccag	tcgggtgagg	ccgttaccc	gtcgttcaag	15060
gggatcatgg	cggcgaagaa	gaagccggtg	gagtcgttg	acctggacga	tctgggtctg	15120
gacgcggacg	aggtcggtct	ggcgggtgcg	tggacggtg	tggattccgc	caccgagcgt	15180
ccggcgcgga	cggcgggcac	gatcgtgaag	gacgagggtg	agggcggcag	gcagctcgcc	15240
gggttcctcg	cgggcccagaa	gttcatctag	tccgcata	tttccccct	gttccctct	15300
ctcgtccccc	cttgtctgg	gtgcgttgc	atggctgaag	ttcttgttct	gtcgtatcac	15360
gtggacggtg	cggtccgcaa	gcccaccc	gagctgtga	cgctggcg	tcgtgtcggt	15420
gaccggtcg	ccgtggtgct	gggtgccggt	gccggggacg	ctgcccgg	gctgggtgag	15480
cacggtgcgg	tgaaggctt	gacctcgac	gccccggagt	tcgcggatta	tctggtgg	15540
ccgaaggctcg	acgcgctgc					15559

<210> 2
<211> 1281
<212> DNA
<213> Streptomyces griseus

<400> 2	atgtctgctg	agtcgcctct	gctgcggctt	tccggcgccg	ggttcgtcct	gccggggccg	60
	gacggccgcg	cctgcaccga	cctggacacc	ttctgggtg	tggtgcgca	cggggcgagc	120
	tgcctctccc	cgtacgccc	tcccgaactc	ccccctccgt	tcgcccggac	cgtgaacggc	180
	tgggacccgg	agaccgaact	cccgctgtcg	gaacggcaga	tacgccc	ctcgccgccc	240
	gggctgatgg	ccacgggtgc	ggtgcaccgg	gcgcgtggagc	acgcgggct	gagcgcggac	300
	gacctcgatc	cggggcgatc	cgcgcgtc	gcctgctc	tccagttc	gttcccggag	360
	accgagcgct	actacgcct	ggcccggac	gaggggg	ccgcctc	catggagta	420
	tggctcaacg	ggaccccgcc	cagtgtgg	ggcacccgt	cctccgg	ccggctgccc	480
	tgccagacgc	tgagcgtgg	gggctcc	aatgtggc	tcgcggac	ccacctcg	540

054030-0031nonactincluster.ST25.txt

cagcagatgt tccgggtgcgg ggacatcgac cgccgcgatcg tcgtcggcgt ggacaccacg 600
gtggaccggg tcttcgtggc aggacccaggc cacaccggac gcagcggcta cccgcgtcc 660
tcgcctctccg acgaccccgc cgacgtccgg ccgcacgacg agatccagac cggcaacgcc 720
accggggagg gcgcgcgtcgc cgtggtgctg gaaaaccggg cggcggaccgg ggaccgccc 780
gggctgctgc accgcgcgca tctgcgcacc tcgcgcctca acggccccctc caccgtggcc 840
accggaccgc cgcacaacgt ggtgggcgac gtactggcca cgctggcttc ggcccggcgc 900
ggcctggcg atctggcggt cgtcaacgac tacgcggacg gcaaccgggtt cgtcgaggac 960
cacctgtgcc aggcgcgtcgc cggggtaag gagggcgccg ggtacggcg ggagctgcgg 1020
ctcaccaacc aggaggcggt ctgcggcat gtcgcggaa ccggcggcct ggtcaaactc 1080
ctcggcagcc tcctcatgct gcgcacggc catatgcccc ccagcgccaa caccctggtc 1140
ccgtacgcgg gtctgcccgg cgacccgggt ctcgcggcg gcctggcgac cggcggagac 1200
agcgcgcctgg tgctcgccctc cggggcgggc ggcgacgcca cgagcatggt catcgaatac 1260
gaaggcggcg acttgccatg a 1281

<210> 3

<211> 426

<212> PRT

<213> Streptomyces griseus

<400> 3

Met Ser Ala Glu Leu Pro Leu Leu Arg Leu Ser Gly Ala Gly Phe Val
1 5 10 15

Leu Pro Gly Pro Asp Gly Arg Ala Cys Thr Asp Leu Asp Thr Phe Trp
20 25 30

Gly Val Val Arg Asp Gly Ala Ser Cys Leu Ser Pro Tyr Ala His Pro
35 40 45

Glu Leu Pro Leu Arg Ile Ala Gly Thr Val Asn Gly Trp Asp Pro Glu
50 55 60

Thr Glu Leu Pro Leu Ser Glu Arg Gln Ile Arg Arg Ser Ser Arg Ala
65 70 75 80

Gly Leu Met Ala Thr Gly Ala Val His Arg Ala Leu Glu His Ala Gly
85 90 95

Leu Ser Ala Asp Asp Leu Asp Pro Gly Arg Thr Ala Leu Val Ala Cys
100 105 110

054030-0031nonactincluster.ST25.txt

Ser Leu Gln Phe Ala Phe Pro Glu Thr Glu Arg Tyr Tyr Ala Leu Ala
115 120 125

Arg Asp Glu Gly Val Ala Ala Leu Gly Met Glu Tyr Trp Leu Asn Gly
130 135 140

Thr Pro Pro Ser Val Val Gly Thr Val Ala Ser Gly Leu Arg Leu Pro
145 150 155 160

Cys Gln Thr Leu Ser Val Ala Gly Ser Cys Asn Val Ala Leu Arg Thr
165 170 175

Leu His Leu Val Gln Gln Met Phe Arg Cys Gly Asp Ile Asp Arg Ala
180 185 190

Ile Val Val Gly Val Asp Thr Thr Val Asp Pro Val Phe Val Ala Gly
195 200 205

Thr Ser His Thr Gly Arg Ser Gly Tyr Arg Ala Ser Ser Leu Ser Asp
210 215 220

Asp Pro Ala Asp Val Arg Pro His Asp Glu Ile Gln Thr Gly Asn Ala
225 230 235 240

Thr Gly Glu Gly Ala Leu Ala Val Val Leu Glu Asn Pro Ala Ala Thr
245 250 255

Gly Asp Arg Pro Gly Leu Leu His Arg Ala His Leu Arg Thr Ser Arg
260 265 270

Ser Asn Gly Pro Ser Thr Val Ala Thr Gly Pro Pro Ala Asn Val Val
275 280 285

Gly Asp Val Leu Ala Thr Leu Ala Ser Ala Arg Arg Gly Leu Gly Asp
290 295 300

Leu Ala Phe Val Asn Asp Tyr Ala Asp Gly Asn Arg Phe Val Glu Asp
305 310 315 320

His Leu Cys Gln Ala Leu Ala Gly Val Lys Glu Ala Ala Gly Tyr Gly
325 330 335

Gly Glu Leu Arg Leu Thr Asn Gln Glu Ala Val Phe Gly His Val Ala
340 345 350

Gly Thr Gly Gly Leu Val Lys Leu Leu Gly Ser Leu Leu Met Leu Arg
355 360 365

054030-0031nonactincluster.ST25.txt

His Gly His Ile Ala Pro Ser Ala Asn Thr Leu Val Pro Tyr Ala Gly
370 375 380

Leu Pro Gly Asp Pro Val Leu Ala Gly Gly Leu Ala Thr Gly Gly Asp
385 390 395 400

Ser Ala Leu Val Leu Ala Ser Gly Ala Gly Gly Asp Ala Thr Ser Met
405 410 415

Val Ile Glu Tyr Glu Gly Gly Asp Leu Pro
420 425

<210> 4

<211> 1278

<212> DNA

<213> Streptomyces griseus

<400> 4

atggggttct gcctgcccgg tgcgggcac gagccgggtgc gcacggccga gcaggtctgg	60
gcggccgcct ccaccgggac cagtcatgtc gaacgcgcacg gcttccacca cgggaccgta	120
cgcgggtccc gcgaggcggtt cggagagctg ctgccggaca taccggcccg ctatctgcgc	180
agctacgccc acgtccaccc tctacgggctg atctcgctgg ccgaggccctg cggggacgccc	240
ggactcgatt acgggaaagg cgagttgaga ggggcggacg tgctgaccgc cggggccggg	300
gtggacagca actacgacag ctaccgcgcc tggcacgacg ccgatccggc gacggtcact	360
ccctcgacg ccaagtccct cttcgtacgg ctcctgggtgg cgggcaccc tcagcgacgtc	420
ggcccccgtcc aggccgcgct gctcggttcc accggcgcca actacacggt gagctgcggc	480
tgcgcctccct cctcggtgct gctcggtatc gccccatga tgatcgccctc cggccagagc	540
gacctggtcg tggtcacccgg ggtggaccgc ttgcacaccg aacgggtgct gcacggacac	600
cgtttcgacg aggtcgatcgac ggcgcgaggc gtgcacgggtgc ggcacaacag cgatccggcg	660
gcagcaccccc gtcacgacccg gccgatgcgc ccgtacgacg cggcgggcga ctgcataaac	720
tacggcgacg ggtcggtgac cctgatccctg gagagccgcg aacacgcgc cgcgcggggc	780
gcccggacgc acggggcggt cctcggtccag gccaccacgc gcggggccct gaacagcgcc	840
gtcgccatcg acaccggcgg tacggggctg gccgaagcgg cccgcccgcgc cctgggcac	900
cataacctcg tggggcgat cccctacgtc aacggggcg ggcggggcga cgcgtgttc	960
acccggatcg agtccaacgc cgtccgcgcc ctgtggggcg accggtccga gcaggtgtcg	1020
gtgagttcgc aggaggcggt cttcggtcac agcggcgccgc cgctcgacaa tctgggcac	1080
gctgcgtacgc tgatgtatgt ggcgcgaggga gaggtctgccc ccacggccaa ctgcgcgacc	1140
ccgtcgcccg tctgcacatt cgaccggcgtc cccggcacca ggacgcgtgc gctggcttc	1200

054030-0031nonactincluster.ST25.txt

gaccggggccc	ttagcttcaa	ctaccaggtg	ggcgggtca	acagcgact	gctgctggga	1260										
ggtggcgatg	tctgctga					1278										
<210>	5															
<211>	425															
<212>	PRT															
<213> Streptomyces griseus																
<400>	5															
Met	Gly	Phe	Cys	Leu	Pro	Gly	Ala	Gly	Asp	Glu	Pro	Val	Arg	Thr	Ala	
1				5				10					15			
Glu	Gln	Val	Trp	Ala	Ala	Ala	Ser	Thr	Gly	Thr	Ser	His	Val	Glu	Arg	
							25					30				
Asp	Gly	Phe	His	His	Gly	Thr	Val	Arg	Gly	Ala	Arg	Glu	Ala	Phe	Gly	
			35			40					45					
Glu	Leu	Leu	Pro	Asp	Ile	Pro	Ala	Arg	Tyr	Leu	Arg	Ser	Tyr	Ala	Asp	
			50			55				60						
Val	His	Leu	Tyr	Gly	Leu	Ile	Ser	Leu	Ala	Glu	Ala	Cys	Arg	Asp	Ala	
			65			70				75			80			
Gly	Leu	Asp	Tyr	Gly	Lys	Gly	Glu	Leu	Arg	Gly	Ala	Asp	Val	Leu	Thr	
			85				90						95			
Ala	Arg	Ala	Gly	Val	Asp	Ser	Asn	Tyr	Asp	Ser	Tyr	Arg	Ala	Trp	His	
			100				105					110				
Asp	Ala	Asp	Pro	Ala	Thr	Val	Thr	Pro	Ser	Asp	Ala	Lys	Ser	Leu	Phe	
			115			120					125					
Val	Arg	Leu	Leu	Val	Ala	Gly	Thr	Ser	Ser	Asp	Val	Gly	Pro	Val	Gln	
			130			135					140					
Ala	Ala	Leu	Leu	Gly	Ser	Thr	Gly	Ala	Asn	Tyr	Thr	Val	Ser	Cys	Gly	
			145			150				155			160			
Cys	Ala	Ser	Ser	Ser	Val	Leu	Leu	Gly	Ile	Ala	Arg	Met	Met	Ile	Ala	
			165			170					175					
Ser	Gly	Gln	Ser	Asp	Leu	Val	Val	Val	Thr	Gly	Val	Asp	Arg	Phe	Asp	
			180			185					190					
Thr	Glu	Arg	Val	Leu	His	Gly	His	Arg	Leu	Arg	Glu	Val	Val	Glu	Arg	
			195			200					205					

054030-0031nonactincluster.ST25.txt

Glu Gly Val Thr Val Arg His Asn Ser Asp Pro Pro Ala Ala Pro Arg
210 215 220

His Asp Arg Pro Met Arg Pro Tyr Asp Ala Ala Gly Asp Cys Met Asn
225 230 235 240

Tyr Gly Asp Gly Ser Val Thr Leu Ile Leu Glu Ser Arg Glu His Ala
245 250 255

Ala Ala Arg Gly Ala Arg Thr His Gly Ala Val Leu Gly Gln Ala Thr
260 265 270

Thr Arg Gly Gly Leu Asn Ser Ala Val Ala Ile Asp Thr Gly Gly Thr
275 280 285

Gly Leu Ala Glu Ala Ala Arg Arg Ala Leu Gly Asp His Thr Ser Leu
290 295 300

Gly Arg Ile Pro Tyr Val Asn Gly Gly Glu Gly Asp Ala Leu Phe
305 310 315 320

Thr Arg Ile Glu Ser Asn Ala Val Arg Ala Leu Trp Gly Asp Arg Ser
325 330 335

Glu Gln Val Leu Val Ser Ser Gln Glu Ala Cys Phe Gly His Ser Gly
340 345 350

Ala Pro Leu Gly Asn Leu Gly Thr Ala Leu Thr Leu Met Met Met Arg
355 360 365

Glu Gly Glu Val Cys Pro Thr Ala Asn Cys Ala Thr Pro Ser Pro Val
370 375 380

Cys Thr Phe Asp Pro Val Pro Gly Thr Arg Thr Arg Ala Leu Gly Phe
385 390 395 400

Asp Arg Ala Leu Ser Phe Asn Tyr Gln Val Gly Gly Val Asn Ser Ala
405 410 415

Leu Leu Leu Gly Gly Asp Val Cys
420 425

<210> 6
<211> 1658

<212> DNA
<213> Streptomyces griseus

<400> 6

054030-0031nonactincluster.ST25.txt

atgtgctcgatccggcgtcc	60
gcgcgcgtgc	
ccacggcgga	
gcagtgctgt	
ctgggtcccc	
tgctcaggcg	120
acgtgccgccc	
gcagcacccgg	
cggcgccgta	
cgcgttcatg	
ccggacggtg	
acctctggac	180
gtacgcgcgc	
accctccggg	
agaccgagga	
gacggccgccc	
gcgctccagg	
cgctgggagt	240
cgtcccgggc	
gaactgggtc	
tgagctggct	
gccccaaacgg	
cccgacgcgc	
tgcgcgcctg	300
gtacggggtc	
aacctggcg	
gcycygtcct	
ggtgcccgtc	
aaacatcgat	
accgggggtgc	360
gatcctgcgt	
caggtgatcg	
ccgacagcgg	
ggccgaggtg	
ctgatctgcc	
ggccgtcgct	420
ggcgccccgg	
ctggaggatt	
cgacgcgc	
ggtggggggcg	
gtgcgcacgg	
tggtcctgct	480
gccggggggcc	
gaggacgcgg	
cccaggacgt	
ggaggcgctc	
gccggggcg	
tggccacgcg	540
cttccgggtg	
gagaccgcac	
tgcgcgcgg	
ccggcgaggag	
ttcgcggagc	
cggtgcccgc	600
ccccggccgc	
tgggaccgc	
agaccgtcat	
ctacaccctcc	
gggacgaccg	
gtccgtccaa	660
gggcgtcg	
tcctcctacg	
cgcacctgta	
cagcagttgc	
accgcccgt	
tccacggcat	720
ggccggaccg	
gaggaccgct	
atctgctgca	
actgcccgt	
ttccacgcgg	
gcggcacgat	780
cggcgcgtac	
gggatgctgg	
tgcacggcg	
ttcggtgacg	
gtcgtgccc	
cgttcaccac	840
cggggagttc	
tggccgctga	
tccggcgac	
ggggacgacc	
ctgtgcacgc	
tgctcggcgt	900
gatggcgacc	
tatctgctca	
agcagccgccc	
gctgcccag	
gacaccgcgc	
acccttgcg	960
ggcggcctac	
gtcatccgt	
tcaccgaggg	
ggcgcacggag	
ttctccaagc	
ggttcgggt	1020
cccggtccgc	
gcgcgttca	
acatgaccg	
ggtgtcggt	
ccgggtct	
ccgcgcgg	1080
ccaccacccg	
ggcgtcccg	
tgcactgcgg	
ggagccccgg	
ccggggatcg	
ccgcgcgggt	1140
cgtcgacgac	
cacgaccggg	
aggtggcg	
cggcgaggcg	
ggcgaactgg	
tgctgcgcgc	1200
ggaccgtccg	
tggtcgttcc	
tgagcggcta	
cctcggccgg	
cccggcgaga	
cggccgcgt	1260
ctggcgcaac	
ggctgggtcc	
acaccgggaa	
cacccctccgc	
cggggccccc	
acggcgggct	1320
ggtcttcgtg	
gaccgcaaga	
aggacgccat	
ccgcaggcgc	
ggcgagaaca	
tctcctcctt	1380
c gaggtggag	
gcgcaggcgg	
tggcccaccc	
gggggtgct	
gaggcggcgg	
cggtggcggt	1440
gcccggcgac	
gagggcgagg	
acgaggtgct	
gctgggtgt	
gcggaccgcg	
acccctcgcc	1500
cccggtcgac	
ccggcgccgc	
tgctggagtt	
cctgcggag	
cggctggccc	
acttcatgt	1560
gccgcgtac	
atccgggtgc	
tgcccgagct	
cccgaagact	
cccaccggca	
agccgaccaa	1620
gcacacgcgt	
cgcgccgagg	
gcgtggtgcc	
ggggacgtgg	
gaccgcgagg	
ccgcgggcat	1658
ccggatacgc	
agggagaaga	
tcgtatga	

<210> 7
<211> 555

<212> PRT

<213> Streptomyces griseus

<400> 7

054030-0031nonactincluster.ST25.txt

Met Ile Asp Asp Val Leu Asp Pro Ala Ser Ala Ala Val Pro Thr Ala
1 5 10 15

Glu Gln Cys Val Leu Gly Pro Leu Leu Arg Arg Arg Ala Ala Ala Ala
20 25 30

Pro Ala Ala Pro Tyr Ala Leu Met Pro Asp Gly Asp Leu Trp Thr Tyr
35 40 45

Ala Arg Thr Leu Arg Glu Thr Glu Glu Thr Ala Ala Ala Leu Gln Ala
50 55 60

Leu Gly Val Val Pro Gly Glu Leu Val Leu Ser Trp Leu Pro Asn Gly
65 70 75 80

Pro Asp Ala Leu Arg Ala Trp Tyr Gly Val Asn Leu Ala Gly Ala Val
85 90 95

Leu Val Pro Leu Asn Ile Ala Tyr Arg Gly Ala Ile Leu Arg Gln Val
100 105 110

Ile Ala Asp Ser Gly Ala Glu Val Leu Ile Cys Arg Pro Ser Leu Ala
115 120 125

Ala Arg Leu Glu Asp Ser Asp Asp Ala Val Gly Ala Val Arg Thr Val
130 135 140

Val Leu Leu Pro Gly Pro Glu Asp Ala Ala Gln Asp Val Glu Ala Leu
145 150 155 160

Ala Gly Arg Leu Ala Thr Arg Phe Arg Val Glu Thr Ala Leu Arg Ala
165 170 175

Asp Arg Ala Glu Phe Ala Glu Pro Val Pro Ala Pro Arg Pro Trp Asp
180 185 190

Pro Gln Thr Val Ile Tyr Thr Ser Gly Thr Thr Gly Pro Ser Lys Gly
195 200 205

Val Val Ser Ser Tyr Ala His Leu Tyr Ser Ser Cys Thr Ala Ala Phe
210 215 220

His Gly Met Ala Gly Pro Glu Asp Arg Tyr Leu Leu Gln Leu Pro Leu
225 230 235 240

Phe His Ala Gly Gly Thr Ile Gly Ala Tyr Gly Met Leu Val His Gly
245 250 255

054030-0031nonactincluster.ST25.txt

Gly Ser Val Thr Val Val Pro Ala Phe Thr Thr Gly Glu Phe Trp Pro
260 265 270

Leu Ile Arg Arg Thr Gly Thr Thr Leu Cys Thr Leu Leu Gly Val Met
275 280 285

Ala Thr Tyr Leu Leu Lys Gln Pro Pro Leu Pro Gln Asp Thr Ala His
290 295 300

Pro Leu Arg Ala Ala Tyr Val Ile Pro Phe Thr Glu Gly Ala Thr Glu
305 310 315 320

Phe Ser Lys Arg Phe Gly Val Pro Val Arg Ala Leu Phe Asn Met Thr
325 330 335

Glu Val Ser Cys Pro Val Leu Ser Ala Pro Asp His His Pro Gly Val
340 345 350

Pro Met His Cys Gly Glu Pro Arg Pro Gly Ile Ala Ala Arg Val Val
355 360 365

Asp Asp His Asp Arg Glu Val Ala Asp Gly Glu Ala Gly Glu Leu Val
370 375 380

Leu Arg Ala Asp Arg Pro Trp Ser Phe Leu Ser Gly Tyr Leu Gly Arg
385 390 395 400

Pro Ala Glu Thr Ala Ala Val Trp Arg Asn Gly Trp Phe His Thr Gly
405 410 415

Asp Thr Phe Arg Arg Ala Pro Asp Gly Gly Leu Val Phe Val Asp Arg
420 425 430

Lys Lys Asp Ala Ile Arg Arg Gly Glu Asn Ile Ser Ser Phe Glu
435 440 445

Val Glu Ala Gln Ala Val Ala His Pro Gly Val Leu Glu Ala Ala Ala
450 455 460

Val Ala Val Pro Gly Asp Glu Gly Glu Asp Glu Val Leu Leu Val Val
465 470 475 480

Ala Asp Arg Asp Pro Ser Ala Pro Val Asp Pro Ala Ala Leu Leu Glu
485 490 495

Phe Leu Arg Glu Arg Leu Ala His Phe Met Leu Pro Arg Tyr Ile Arg

054030-0031nonactincluster.ST25.txt

500

505

510

Val Leu Pro Glu Leu Pro Lys Thr Pro Thr Gly Lys Pro Thr Lys His
515 520 525

Thr Leu Arg Ala Glu Gly Val Val Ala Gly Thr Trp Asp Arg Glu Ala
530 535 540

Ala Gly Ile Arg Ile Arg Arg Glu Lys Ile Val
545 550 555